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RAW SEQUENCE LISTING

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Application Serial Number: 10/519,947
Source: PCT/10
Date Processed by STIC: 1/13/06

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PCT

RAW SEQUENCE LISTING

DATE: 01/13/2006

PATENT APPLICATION: US/10/519,947

TIME: 10:35:49

Input Set : A:\Final sequence list-12810-00141-US.txt

Output Set: N:\CRF4\01132006\J519947.raw

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3 <110> APPLICANT: Andersson, Mariette
4   Trifonova, Adelina
5   Hofvander, Per
7 <120> TITLE OF INVENTION: Use of AHAS mutant genes as selection marker in potato
8   transformation
10 <130> FILE REFERENCE: 12810-00141-US
12 <140> CURRENT APPLICATION NUMBER: US 10/519,947
13 <141> CURRENT FILING DATE: 2004-12-29
15 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/007085
16 <151> PRIOR FILING DATE: 2003-07-03
18 <150> PRIOR APPLICATION NUMBER: EP 02015247.6
19 <151> PRIOR FILING DATE: 2002-07-09
21 <160> NUMBER OF SEQ ID NOS: 2
23 <170> SOFTWARE: PatentIn version 3.3
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27 <211> LENGTH: 5717
28 <212> TYPE: DNA
29 <213> ORGANISM: Arabidopsis thaliana
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46 acataagtaa ttaagttgta caactttttt ttaatgaaaa gagagagtaa atttatcatg 360
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60 caaaaaaaaa caaggagtct tgtcttcgtt ctcaaatttc agagctcttg cacttttcaa 780
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74 cctctcagag atttcgctaa gagcagtggt cgtctcgtcc agcgtgtgca caaaccgat 1200
76 cgcaagggtg acgccttttc tcaaaaaaat ctcatctccg atttttgatc tgtagattag 1260

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118 cttgctcatc tttctctga acc atg gcg gcg gca aca aca aca aca aca 2513
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120 1 5 10
122 tct tct tcg atc tcc ttc tcc acc aaa cca tct cct tcc tcc tcc aaa 2561
123 Ser Ser Ser Ile Ser Phe Ser Thr Lys Pro Ser Pro Ser Ser Ser Lys
124 15 20 25
126 tca cca tta cca atc tcc aga ttc tcc ctc cca ttc tcc cta aac ccc 2609
127 Ser Pro Leu Pro Ile Ser Arg Phe Ser Leu Pro Phe Ser Leu Asn Pro
128 30 35 40
130 aac aaa tca tcc tcc tcc tcc cgc cgc cgc ggt atc aaa tcc agc tct 2657
131 Asn Lys Ser Ser Ser Ser Ser Arg Arg Arg Gly Ile Lys Ser Ser Ser
132 45 50 55
134 ccc tcc tcc atc tcc gcc gtg ctc aac aca acc acc aat gtc aca acc 2705
135 Pro Ser Ser Ile Ser Ala Val Leu Asn Thr Thr Thr Asn Val Thr Thr
136 60 65 70
138 act ccc tct cca acc aaa cct acc aaa ccc gaa aca ttc atc tcc cga 2753
139 Thr Pro Ser Pro Thr Lys Pro Thr Lys Pro Glu Thr Phe Ile Ser Arg
140 75 80 85 90
142 ttc gct cca gat caa ccc cgc aaa ggc gct gat atc ctc gtc gaa gct 2801
143 Phe Ala Pro Asp Gln Pro Arg Lys Gly Ala Asp Ile Leu Val Glu Ala
144 95 100 105
146 tta gaa cgt caa ggc gta gaa acc gta ttc gct tac cct gga ggt gca 2849
147 Leu Glu Arg Gln Gly Val Glu Thr Val Phe Ala Tyr Pro Gly Gly Ala
148 110 115 120
150 tca atg gag att cac caa gcc tta acc cgc tct tcc tca atc cgt aac 2897
151 Ser Met Glu Ile His Gln Ala Leu Thr Arg Ser Ser Ser Ile Arg Asn
152 125 130 135
154 gtc ctt cct cgt cac gaa caa gga ggt gta ttc gca gca gaa gga tac 2945
155 Val Leu Pro Arg His Glu Gln Gly Gly Val Phe Ala Ala Glu Gly Tyr

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159	Ala Arg Ser Ser Gly Lys Pro Gly Ile Cys Ile Ala Thr Ser Gly Pro			
160	155 160 165 170			
162	gga gct aca aat ctg gtt agc gga tta gcc gat gcg ttg tta gat agt	3041		
163	Gly Ala Thr Asn Leu Val Ser Gly Leu Ala Asp Ala Leu Leu Asp Ser			
164	175 180 185			
166	gtt cct ctt gta gca atc aca gga caa gtc cct cgt cgt atg att ggt	3089		
167	Val Pro Leu Val Ala Ile Thr Gly Gln Val Pro Arg Arg Met Ile Gly			
168	190 195 200			
170	aca gat gcg ttt caa gag act ccg att gtt gag gta acg cgt tcg att	3137		
171	Thr Asp Ala Phe Gln Glu Thr Pro Ile Val Glu Val Thr Arg Ser Ile			
172	205 210 215			
174	acg aag cat aac tat ctt gtg atg gat gtt gaa gat atc cct agg att	3185		
175	Thr Lys His Asn Tyr Leu Val Met Asp Val Glu Asp Ile Pro Arg Ile			
176	220 225 230			
178	att gag gaa gct ttc ttt tta gct act tct ggt aga cct gga cct gtt	3233		
179	Ile Glu Glu Ala Phe Phe Leu Ala Thr Ser Gly Arg Pro Gly Pro Val			
180	235 240 245 250			
182	ttg gtt gat gtt cct aaa gat att caa caa cag ctt gcg att cct aat	3281		
183	Leu Val Asp Val Pro Lys Asp Ile Gln Gln Gln Leu Ala Ile Pro Asn			
184	255 260 265			
186	tgg gaa cag gct atg aga tta cct ggt tat atg tct agg atg cct aaa	3329		
187	Trp Glu Gln Ala Met Arg Leu Pro Gly Tyr Met Ser Arg Met Pro Lys			
188	270 275 280			
190	cct ccg gaa gat tct cat ttg gag cag att gtt agg ttg att tct gag	3377		
191	Pro Pro Glu Asp Ser His Leu Glu Ile Val Arg Leu Ile Ser Glu			
192	285 290 295			
194	tct aag aag cct gtg ttg tat gtt ggt ggt ggt tgt ttg aat tct agc	3425		
195	Ser Lys Lys Pro Val Leu Tyr Val Gly Gly Gly Cys Leu Asn Ser Ser			
196	300 305 310			
198	gat gaa ttg ggt agg ttt gtt gag ctt acg ggg atc cct gtt gcg agt	3473		
199	Asp Glu Leu Gly Arg Phe Val Glu Leu Thr Gly Ile Pro Val Ala Ser			
200	315 320 325 330			
202	acg ttg atg ggg ctg gga tct tat cct tgt gat gat gag ttg tcg tta	3521		
203	Thr Leu Met Gly Leu Gly Ser Tyr Pro Cys Asp Asp Glu Leu Ser Leu			
204	335 340 345			
206	cat atg ctt gga atg cat ggg act gtg tat gca aat tac gct gtg gag	3569		
207	His Met Leu Gly Met His Gly Thr Val Tyr Ala Asn Tyr Ala Val Glu			
208	350 355 360			
210	cat agt gat ttg ttg ttg gcg ttt ggg gta agg ttt gat gat cgt gtc	3617		
211	His Ser Asp Leu Leu Leu Ala Phe Gly Val Arg Phe Asp Asp Arg Val			
212	365 370 375			
214	acg ggt aag ctt gag gct ttt gct agt agg gct aag att gtt cat att	3665		
215	Thr Gly Lys Leu Glu Ala Phe Ala Ser Arg Ala Lys Ile Val His Ile			
216	380 385 390			
218	gat. att gac tcg gct gag att ggg aag aat aag act cct cat gtg tct	3713		
219	Asp Ile Asp Ser Ala Glu Ile Gly Lys Asn Lys Thr Pro His Val Ser			
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226 gag aac cga gcg gag gag ctt aag ctt gat ttt gga gtt tgg agg aat 3809
227 Glu Asn Arg Ala Glu Glu Leu Lys Leu Asp Phe Gly Val Trp Arg Asn
228          430          435          440
230 gag ttg aac gta cag aaa cag aag ttt ccg ttg agc ttt aag acg ttt 3857
231 Glu Leu Asn Val Gln Lys Gln Lys Phe Pro Leu Ser Phe Lys Thr Phe
232          445          450          455
234 ggg gaa gct att cct cca cag tat gcg att aag gtc ctt gat gag ttg 3905
235 Gly Glu Ala Ile Pro Pro Gln Tyr Ala Ile Lys Val Leu Asp Glu Leu
236          460          465          470
238 act gat gga aaa gcc ata ata agt act ggt gtc ggg caa cat caa atg 3953
239 Thr Asp Gly Lys Ala Ile Ile Ser Thr Gly Val Gly Gln His Gln Met
240 475          480          485          490
242 tgg gcg gcg cag ttc tac aat tac aag aaa cca agg cag tgg cta tca 4001
243 Trp Ala Ala Gln Phe Tyr Asn Tyr Lys Lys Pro Arg Gln Trp Leu Ser
244          495          500          505
246 tca gga ggc ctt gga gct atg gga ttt gga ctt cct gct gcg att gga 4049
247 Ser Gly Gly Leu Gly Ala Met Gly Phe Gly Leu Pro Ala Ala Ile Gly
248          510          515          520
250 gcg tct gtt gct aac cct gat gcg ata gtt gtg gat att gac gga gat 4097
251 Ala Ser Val Ala Asn Pro Asp Ala Ile Val Val Asp Ile Asp Gly Asp
252          525          530          535
254 gga agc ttt ata atg aat gtg caa gag cta gcc act att cgt gta gag 4145
255 Gly Ser Phe Ile Met Asn Val Gln Glu Leu Ala Thr Ile Arg Val Glu
256          540          545          550
258 aat ctt cca gtg aag gta ctt tta tta aac aac cag cat ctt ggc atg 4193
259 Asn Leu Pro Val Lys Val Leu Leu Leu Asn Asn Gln His Leu Gly Met
260 555          560          565          570
262 gtt atg caa tgg gaa gat cgg ttc tac aaa gct aac cga gct cac aca 4241
263 Val Met Gln Trp Glu Asp Arg Phe Tyr Lys Ala Asn Arg Ala His Thr
264          575          580          585
266 ttt ctc ggg gat ccg gct cag gag gac gag ata ttc ccg aac atg ttg 4289
267 Phe Leu Gly Asp Pro Ala Gln Glu Asp Glu Ile Phe Pro Asn Met Leu
268          590          595          600
270 ctg ttt gca gca gct tgc ggg att cca gcg gcg agg gtg aca aag aaa 4337
271 Leu Phe Ala Ala Ala Cys Gly Ile Pro Ala Ala Arg Val Thr Lys Lys
272          605          610          615
274 gca gat ctc cga gaa gct att cag aca atg ctg gat aca cca gga cct 4385
275 Ala Asp Leu Arg Glu Ala Ile Gln Thr Met Leu Asp Thr Pro Gly Pro
276          620          625          630
278 tac ctg ttg gat gtg att tgt ccg cac caa gaa cat gtg ttg ccg atg 4433
279 Tyr Leu Leu Asp Val Ile Cys Pro His Gln Glu His Val Leu Pro Met
280 635          640          645          650
282 atc ccg aat ggt ggc act ttc aac gat gtc ata acg gaa gga gat ggc 4481
283 Ile Pro Asn Gly Gly Thr Phe Asn Asp Val Ile Thr Glu Gly Asp Gly
284          655          660          665
286 cgg att aaa tac tgagagatga aaccggtgat tatcagaacc ttttatggtc 4533

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287 Arg Ile Lys Tyr

288 670

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294 ttgtttgggt tcctttcttt cattttataa ataaataatc cggttcgggt tactccttgt 4713
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331 <210> SEQ ID NO: 2

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333 <212> TYPE: PRT

334 <213> ORGANISM: Arabidopsis thaliana

336 <400> SEQUENCE: 2

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343 Arg Phe Ser Leu Pro Phe Ser Leu Asn Pro Asn Lys Ser Ser Ser Ser
344 35 40 45
346 Ser Arg Arg Arg Gly Ile Lys Ser Ser Ser Pro Ser Ser Ile Ser Ala
347 50 55 60
349 Val Leu Asn Thr Thr Thr Asn Val Thr Thr Thr Pro Ser Pro Thr Lys
350 65 70 75 80
352 Pro Thr Lys Pro Glu Thr Phe Ile Ser Arg Phe Ala Pro Asp Gln Pro
353 85 90 95
355 Arg Lys Gly Ala Asp Ile Leu Val Glu Ala Leu Glu Arg Gln Gly Val
356 100 105 110
358 Glu Thr Val Phe Ala Tyr Pro Gly Gly Ala Ser Met Glu Ile His Gln
359 115 120 125
361 Ala Leu Thr Arg Ser Ser Ser Ile Arg Asn Val Leu Pro Arg His Glu
362 130 135 140
364 Gln Gly Gly Val Phe Ala Ala Glu Gly Tyr Ala Arg Ser Ser Gly Lys
365 145 150 155 160
367 Pro Gly Ile Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
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VERIFICATION SUMMARY

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